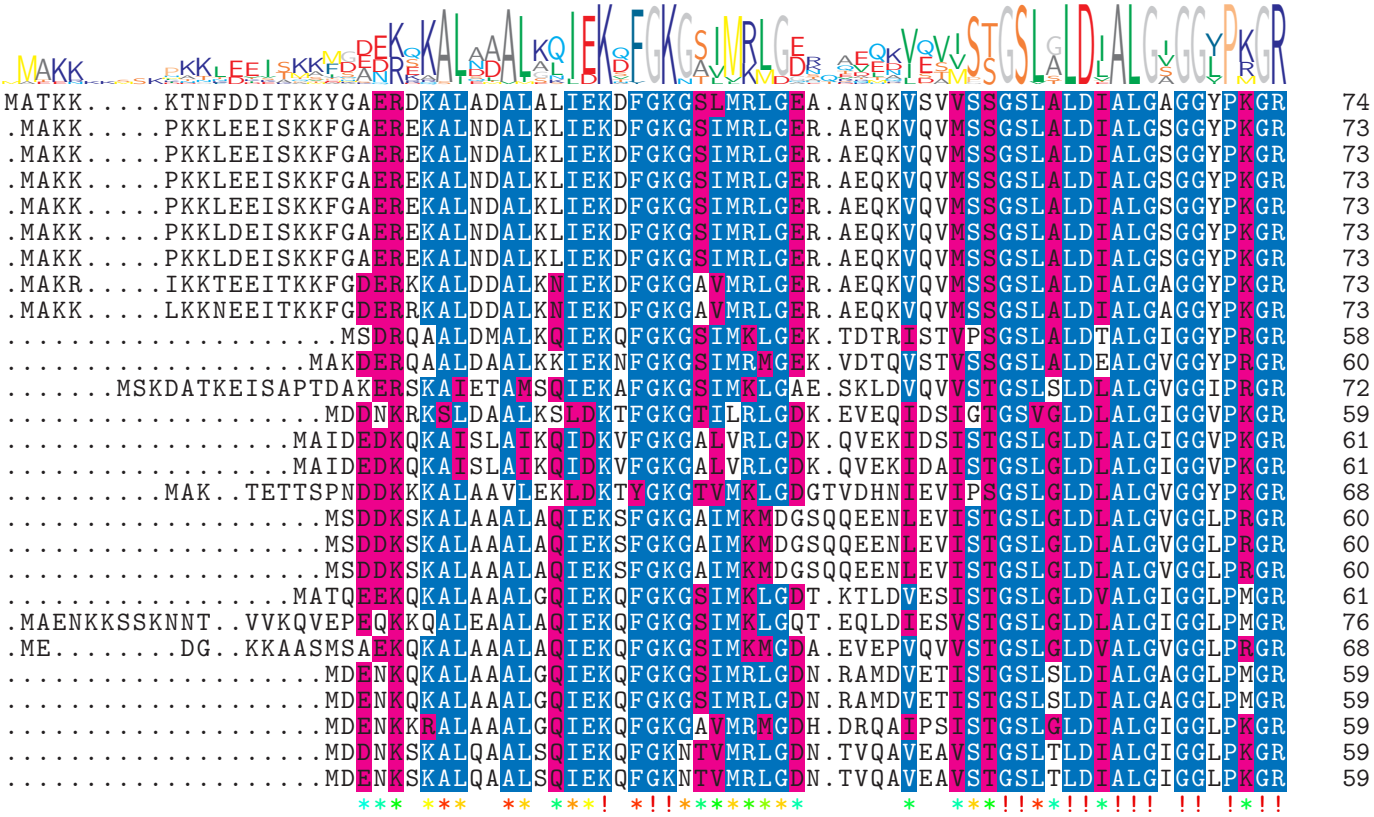
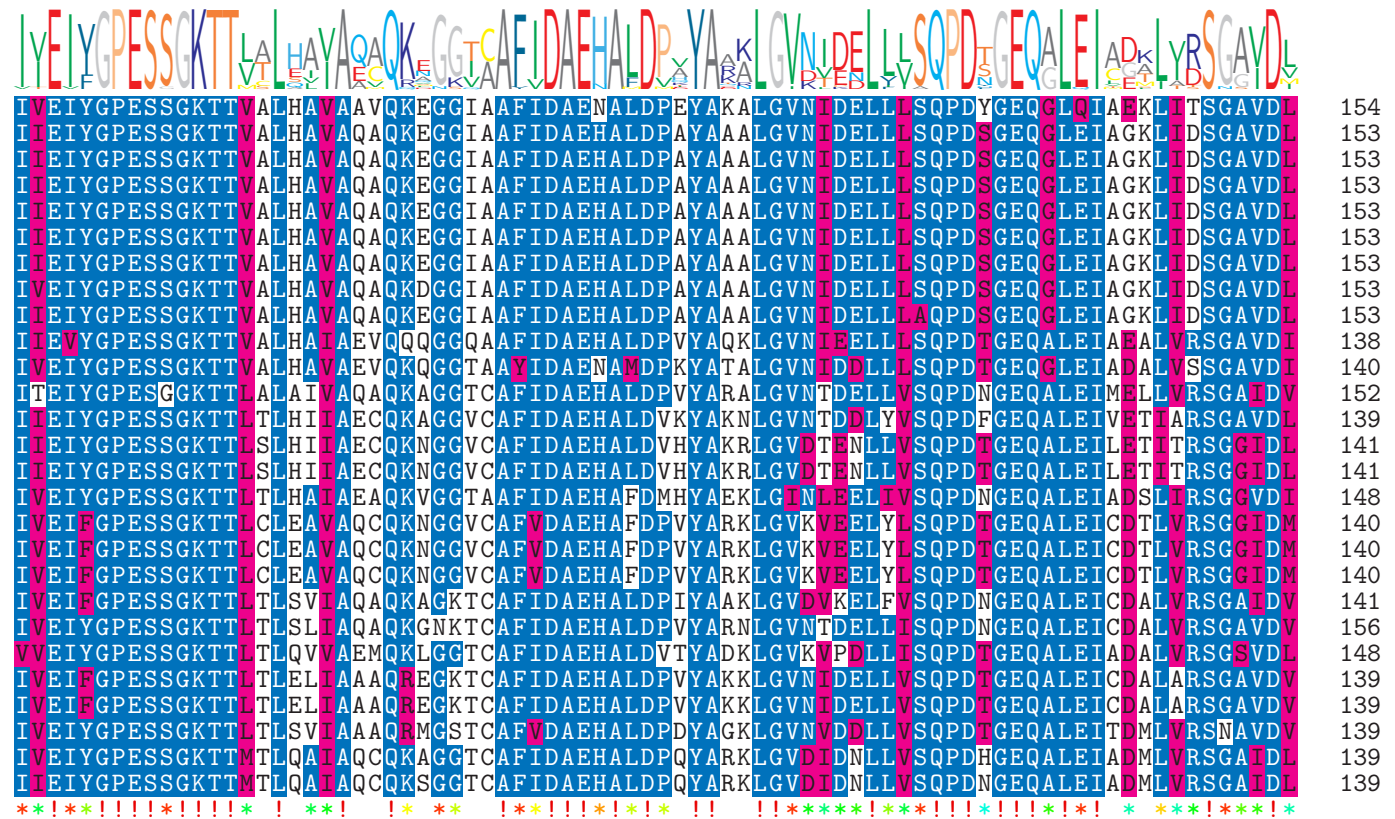


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consensus



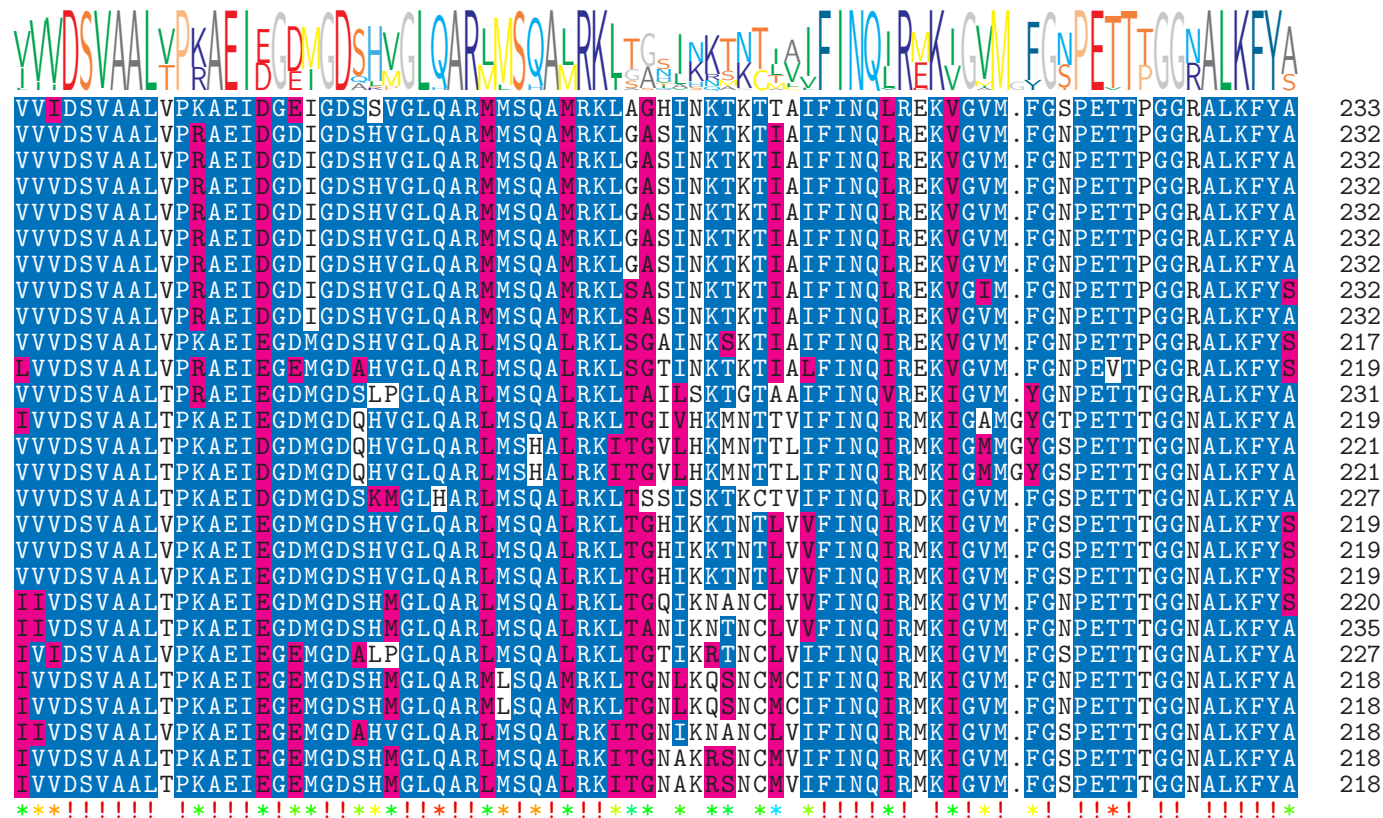
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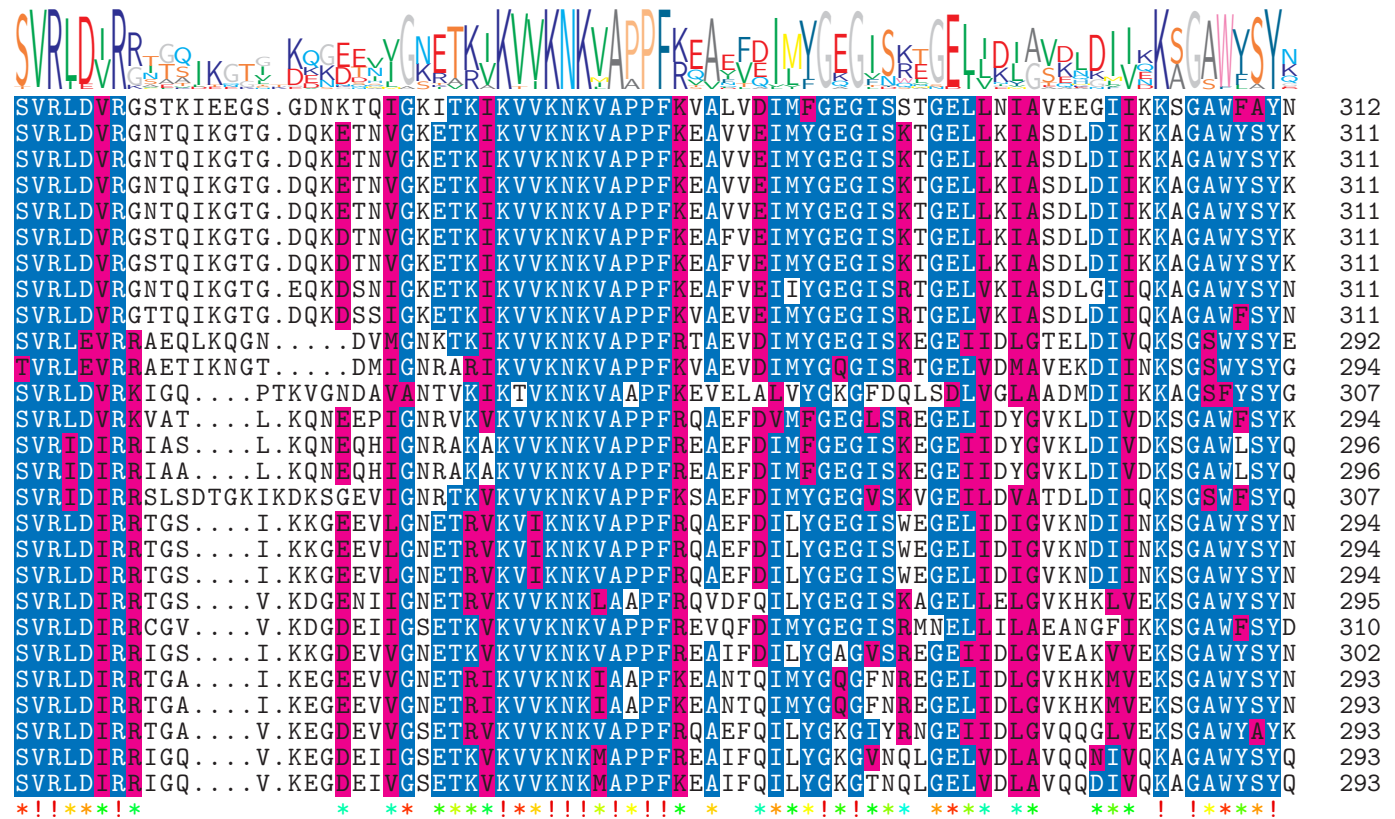
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consensus

Sequence	Score
DEKIGGGA ⁺ E ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FDEI ⁺ DHKV ⁺ RAAH ⁺ CI ⁺ LDDSEVAETE.EETTASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEI ⁺ DKQV ⁺ RSKF ⁺ CLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEI ⁺ DKQV ⁺ RSKF ⁺ CLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEI ⁺ DKQV ⁺ RSKF ⁺ CLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEI ⁺ FDEI ⁺ DKQV ⁺ RSKF ⁺ CLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGS ⁺ ENAK ⁺ KYLAD ⁺ NPEI ⁺ FDEI ⁺ DHQR ⁺ VRVQ ⁺ FCLIDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEI	380
DEKIGQGS ⁺ ENAK ⁺ KYLAD ⁺ NPEI ⁺ FDEI ⁺ DHQR ⁺ VRVQ ⁺ FCLIDGEEIAES....KKDE....VAQVDS..VNEEVPLDLGDELEI	380
GEKIGQGS ⁺ ENAK ⁺ KFLAD ⁺ NPEI ⁺ FDDI ⁺ DHKV ⁺ RVQY ⁺ CLIEEDNTEEKQ.SSKEK.....ETDEK..ADKNLVLELDDTIEL	381
GEKIGQGS ⁺ ENAK ⁺ KRYLAD ⁺ HQP ⁺ LFDEI ⁺ DRKV ⁺ RVKF ⁺ CLLEESSEESAM.AVASE.....E.....TDDLALDLNGLIEI	376
EE ⁺ RL ⁺ GGGREN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQA.EETQEEL.EFE.E.....	348
SERIGGQREN ⁺ AK ⁺ NYLAD ⁺ HED ⁺ VE ⁺ DEV ⁺ RLKV ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPT.TEDE.QI.NILPDDST....EE.....	355
DERIGGQKE ⁺ KTIA ⁺ YIA ⁺ ER ⁺ PEME ⁺ QE ⁺ IRDR ⁺ VMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
DKKLGGGREN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PEI ⁺ ADEIT ⁺ TKAT ⁺ IQNSM ⁺ TEGMISGS..EDDEGE..E.....	343
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KALADEIT ⁺ TLKIK ⁺ ESIG ⁺ SNEEIMPL..PDEPLE..EME.....	347
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KALADEIT ⁺ TLKIK ⁺ ESIG ⁺ SNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRD ⁺ TVKEL ⁺ IKD ⁺ NPEI ⁺ AE ⁺ ELE ⁺ AKI ⁺ REKLQAK.....	343
GAKIGQGKD ⁺ NVRV ⁺ WLKEN ⁺ PEIS ⁺ DEID ⁺ AKIRALN ⁺ GVEMHITEG..T...QD...ETDGE.RPEE.....	348
GAKIGQGKD ⁺ NVRV ⁺ WLKEN ⁺ PEIS ⁺ DEID ⁺ AKIRALN ⁺ GVEMHITEG..T...QD...ETDGE.RPEE.....	348
GAKIGQGKD ⁺ NVRV ⁺ WLKEN ⁺ PEIS ⁺ DEID ⁺ AKIRALN ⁺ GVEMHITEG..T...QD...ETDGE.RPEE.....	348
GEKIGQGGK ⁺ ANS ⁺ MKW ⁺ LNEN ⁺ IEKS ⁺ DELEAR ⁺ LRAELVANPEQALM..ADIEQSENNTESSEDFE.....	354
GTKIGQGGK ⁺ NNAV ⁺ KWLKEN ⁺ PEIAD ⁺ KLQE ⁺ IRNTL ⁺ ASNPNSVLK..ATASDSND ⁺ ESDVE.EFSE....EEL.....	372
GE ⁺ RI ⁺ GGGRDNC ⁺ REFL ⁺ REN ⁺ AE ⁺ LARE ⁺ ENK ⁺ VR ⁺ REHL ⁺ CVTPMGAV..TLAEEVEED.....	352
GD ⁺ KIGQGGK ⁺ ANACK ⁺ YLKEN ⁺ PEIA ⁺ KTLD ⁺ KKL ⁺ REMLLNPNEMQLI..AETSSAAD ⁺ VEFGAVPE.....EF.....	354
GD ⁺ KIGQGGK ⁺ ANACK ⁺ YLKEN ⁺ PEIA ⁺ KTLD ⁺ KKL ⁺ REMLLNPNEMQLI..AETSSAAD ⁺ VEFGAVPE.....EF.....	354
GSKIGQGGK ⁺ ANA ⁺ AKY ⁺ LEEN ⁺ PEI ⁺ GQ ⁺ EIE ⁺ QQI ⁺ IRAKLL ⁺ YTSANTKA..TPVAEDLADADI.....	347
GN ⁺ KIGQGGK ⁺ NNVIR ⁺ YLEEN ⁺ PEI ⁺ QISTE ⁺ IE ⁺ AVI ⁺ REQLLT ⁺ KASDQTA..A.HDETEEE ⁺ PDLL..ES.....	349
GN ⁺ KIGQGGK ⁺ NNVIR ⁺ YLEEN ⁺ PEI ⁺ QIAE ⁺ IE ⁺ ERN ⁺ IREQLLT ⁺ TGTNGAV..Q.I.EDEEE ⁺ PDLL..LE.....S.....	349

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consensus					

-  non conserved
-  similar
-  ≥ 50% conserved